



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/645,085  
Source: TPW  
Date Processed by STIC: 11/17/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/645,085</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input checked="" type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input checked="" type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/645,085

DATE: 11/17/2003

TIME: 15:15:50

Input Set : A:\PTO.YF.txt  
 Output Set: N:\CRF4\11172003\J645085.raw

3 <110> APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA  
 W--> 4 <120> TITLE OF INVENTION: Agonist antibody  
 W--> 5 <130> FILE REFERENCE: FP1009  
 E--> 6 <140> CURRENT APPLICATION NUMBER: US/10/645,085  
 C--> 6 <141> CURRENT FILING DATE: 2002-10-07  
 7 <150> PRIOR APPLICATION NUMBER: JP2000-115246  
 8 <151> PRIOR FILING DATE: 2000-04-17  
 9 <150> PRIOR APPLICATION NUMBER: JP2000-321821  
 10 <151> PRIOR FILING DATE: 2000-10-20  
 11 <150> PRIOR APPLICATION NUMBER: JP2000-321822  
 12 <151> PRIOR FILING DATE: 2000-10-20  
 13 <150> PRIOR APPLICATION NUMBER: PCT/JP01/01912  
 14 <151> PRIOR FILING DATE: 2001-03-12  
 E--> 16 <160> NUMBER OF SEQ ID NOS: 109

PYI! all nucleotides  
 MUST be in  
lower-case letters  
 pp 1-5

92 (p.5)

## ERRORED SEQUENCES

1210 <210> SEQ ID NO: 60  
 1211 <211> LENGTH: 115 108 shown below  
 1212 <212> TYPE: DNA  
 1213 <213> ORGANISM: Artificial Sequence

W--> 1214 <220> FEATURE:  
 1215 <223> OTHER INFORMATION: 12B5VH-4

W--> 1216 <400> SEQUENCE: 60  
 1217 actcgagacg gtgaccatgg tcccttggcc ccagatatcg aaaccataat gttcttcctat 60  
 E--> 1218 cgcacagtaa tacacagccg tgcctcgcc ttcaggctg ttcatttg 108

1238 <210> SEQ ID NO: 63  
 1239 <211> LENGTH: 433 432 (p.2)  
 1240 <212> TYPE: DNA  
 1241 <213> ORGANISM: Human

W--> 1242 <220> FEATURE:

1243 <221> NAME/KEY: CDS  
 1244 <222> LOCATION: (12)...(419)  
 1245 <223> OTHER INFORMATION: HEF-12B5H-g gamma. 12-419 peptide

W--> 1246 <400> SEQUENCE: 63

1247 aagttccac c atg gag ttt ggg ctg aqc tgg gtt ttc ctc gtt gct ctt tta aga 56  
 1248 Met MET Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg  
 1249 1 5 10 15  
 1250 ggt gtc cag tgt cag ctg cag gtq cag tct qgg gga ggc ttq gtc Cgg CCC GGG GGG 116  
 1251 Gly Val Gln Cys Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Arg Pro Gly Gly  
 1252 20 25 30 35  
 1253 tcc ctg agt ctc tcc tgt gca gtc tct gga atc acc ctc agg acc tac ggc atg cac tqg 176

Per 1.822 of sequence  
 Rule, a maximum of 16  
 codons per line  
 insert  
 a hard  
 return  
 after 16<sup>th</sup>  
 codon

16 codons MAXIMUM per line (Please edit)

16 Codons per line only

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/645,085

DATE: 11/17/2003  
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Input Set : A:\PTO.YF.txt  
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✓ Met

1254 Ser Leu Ser Leu Ser Cys Ala Val Ser Gly Ile Thr Leu Arg Thr Tyr Gly MET His Trp  
1255 40 45 50 55  
1256 gtc cgc caq gct cca ggc aag ggg ctg gag tgg qtg gca ggt ata tcc ttt gac gga aga 236  
1257 Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile Ser Phe Asp Gly Arg  
1258 60 65 70 75  
1259 agt gaa tac tat gca gac tcc qtg cag ggc cga ttc acc atc tcc aga gac agt tcc aag 296  
1260 Ser Glu Tyr Tyr Ala Asp Ser Val Gln Gly Arg Phe Thr Ile Ser Arg Asp Ser Ser Lys  
1261 80 85 90 95  
1262 aac acc ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 356  
1263 Asn Thr Leu Tyr Leu Gln MET Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
1264 100 105 110 115  
1265 gcg aga gga gca cat tat ggt ttc gat atc tgg ggc caa ggg aca ate gtc acc gtc tcg 416  
1266 Ala Arg Gly Ala His Tyr Gly Phe Asp Ile Trp Gly Gln Gly Thr MET Val Thr Val Ser  
1267 120 125 130 135

E--> 1268 agt ggtgagtggaa tcc 433

E--> 1269 Ser

1271 <210> SEQ ID NO: 64

1272 <211> LENGTH: (323) 321

1273 <212> TYPE: DNA

1274 <213> ORGANISM: Human

W--> 1275 <220> FEATURE:

1276 <221> NAME/KEY: CDS

1277 <222> LOCATION: (1)...(323)

1278 <223> OTHER INFORMATION: 12B5LV. 1-323 peptide

W--> 1279 <400> SEQUENCE: 64

1280 gac atc cag atg acc cag tct cct acc ctg tct gca tct att gga gac aga gtc acc 60  
1281 Asp Ile Gln MET Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly Asp Arg Val Thr  
1282 5 10 15 20  
1283 atc acc tgc cgg qcc agc gag ggt att tat cac tgg ttg gcc tgg tat cag cag aag cca 120  
1284 Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln Lys Pro  
1285 25 30 35 40  
1286 ggg aaa gcc cct aaa ctc ctg atc tat aag gcc tct agt tta gcc agt ggg gcc cca tca 180  
1287 Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Ala Ser Gly Ala Pro Ser  
1288 45 50 55 60  
1289 agg ttc agc ggc agt gga tct ggg aca gat ttc act ctc acc atc agc ctg cag cct 240  
1290 Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
1291 65 70 75 80  
1292 gat gat ttt gca act tat tac tgc caa caa tat agt aat tat ccg ctc act ttc ggc gga 300  
1293 Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Leu Thr Phe Gly Gly  
1294 85 90 95 100

E--> 1295 ggg acc aag ctg gag atc aaa 323 321

1296 Gly Thr Lys Leu Glu Ile Lys

E--> 1297 105

1344 <210> SEQ ID NO: 69

1345 <211> LENGTH: (110) 102 (p3)

1346 <212> TYPE: DNA

1347 <213> ORGANISM: Artificial Sequence

W--> 1348 <220> FEATURE:

1349 <223> OTHER INFORMATION: 12B5VI,-4

16 codons per line

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/645,085

DATE: 11/17/2003  
TIME: 15:15:50

Input Set : A:\PTO.YF.txt  
Output Set: N:\CRF4\11172003\J645085.raw

W--> 1350 <400> SEQUENCE: 69  
1351 accatcaqca gcctgcagcc tcatgatttt gcaacttatt actgccaaca atatacgtaat 60  
E--> 1352 tatccgctca ctttcggcgg agggaccaag ctggagatca aa 102 ←

Edit all sequences in which  
More than 16 codons per line  
are shown

See pp 4-5 for more info

10/645, 085

4

<400> 6

atg gaa tgg agc tgg ata ttt ctc ttc ctc ctg tca gga act gca	45
Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala	
5 10 15	
ggt gtc cac tcc cag gtc cag ctg cag cag tct gga cct gac ctg	90
Gly Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Asp Leu	
10 20 25 30	
gta aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga	135
Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly	
35 40 45	

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5

<210> 72 *last sequence in submitted file*

<211> 415

<212> DNA

<213> Human

<220>

<221> CDS

<222> (12) ... (398)

<223> HEF-12B5H-g kappa. 12-398 peptide

<400> 72

aagcttccac c atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc 56  
MET Asp MET Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu  
1 5 10 15

tgg ctc cca ggt gcc aaa tgt gac atc cag atg acc cag tct cct tcc acc ctg tct gca  
116

116

(format error)

see item 1 on Error Summary Sheet

This error appears throughout sequence 72

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/645,085

DATE: 11/17/2003  
TIME: 15:15:51

Input Set : A:\PTO.YF.txt  
Output Set: N:\CRF4\11172003\J645085.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:55; Line(s) 1148,1151,1154,1157,1160  
Seq#:63; Line(s) 1250,1251,1253,1254,1256,1257,1259,1260,1262,1263,1265  
Seq#:63; Line(s) 1266  
Seq#:64; Line(s) 1280,1283,1286,1289,1292  
Seq#:65; Line(s) 1308  
Seq#:72; Line(s) 1384,1385,1387,1388,1390,1391,1393,1394,1396,1397

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/645,085

DATE: 11/17/2003

TIME: 15:15:51

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\11172003\J645085.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier  
L:5 M:283 W: Missing Blank Line separator, <130> field identifier  
L:6 M:282 E: Numeric Field Identifier Missing, <140> CURRENT APPLICATION NUMBER: is Added.  
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:22 M:283 W: Missing Blank Line separator, <220> field identifier  
L:24 M:283 W: Missing Blank Line separator, <400> field identifier  
L:31 M:283 W: Missing Blank Line separator, <220> field identifier  
L:33 M:283 W: Missing Blank Line separator, <400> field identifier  
L:40 M:283 W: Missing Blank Line separator, <220> field identifier  
L:42 M:283 W: Missing Blank Line separator, <400> field identifier  
L:49 M:283 W: Missing Blank Line separator, <220> field identifier  
L:51 M:283 W: Missing Blank Line separator, <400> field identifier  
L:58 M:283 W: Missing Blank Line separator, <220> field identifier  
I:62 M:283 W: Missing Blank Line separator, <400> field identifier  
L:95 M:283 W: Missing Blank Line separator, <220> field identifier  
L:99 M:283 W: Missing Blank Line separator, <400> field identifier  
L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6  
L:134 M:283 W: Missing Blank Line separator, <220> field identifier  
L:138 M:283 W: Missing Blank Line separator, <400> field identifier  
L:171 M:283 W: Missing Blank Line separator, <220> field identifier  
L:175 M:283 W: Missing Blank Line separator, <400> field identifier  
L:210 M:283 W: Missing Blank Line separator, <220> field identifier  
L:212 M:283 W: Missing Blank Line separator, <400> field identifier  
L:219 M:283 W: Missing Blank Line separator, <220> field identifier  
L:221 M:283 W: Missing Blank Line separator, <400> field identifier  
L:228 M:283 W: Missing Blank Line separator, <220> field identifier  
L:230 M:283 W: Missing Blank Line separator, <400> field identifier  
L:237 M:283 W: Missing Blank Line separator, <220> field identifier  
L:239 M:283 W: Missing Blank Line separator, <400> field identifier  
L:246 M:283 W: Missing Blank Line separator, <220> field identifier  
L:248 M:283 W: Missing Blank Line separator, <400> field identifier  
L:255 M:283 W: Missing Blank Line separator, <220> field identifier  
L:257 M:283 W: Missing Blank Line separator, <400> field identifier  
L:264 M:283 W: Missing Blank Line separator, <220> field identifier  
L:266 M:283 W: Missing Blank Line separator, <400> field identifier  
L:273 M:283 W: Missing Blank Line separator, <220> field identifier  
L:275 M:283 W: Missing Blank Line separator, <400> field identifier  
L:282 M:283 W: Missing Blank Line separator, <220> field identifier  
L:284 M:283 W: Missing Blank Line separator, <400> field identifier  
L:291 M:283 W: Missing Blank Line separator, <220> field identifier  
L:293 M:283 W: Missing Blank Line separator, <400> field identifier  
L:300 M:283 W: Missing Blank Line separator, <220> field identifier  
L:302 M:283 W: Missing Blank Line separator, <400> field identifier  
L:311 M:283 W: Missing Blank Line separator, <220> field identifier  
L:315 M:283 W: Missing Blank Line separator, <400> field identifier  
L:377 M:283 W: Missing Blank Line separator, <220> field identifier  
L:379 M:283 W: Missing Blank Line separator, <400> field identifier  
L:386 M:283 W: Missing Blank Line separator, <220> field identifier

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/645,085

DATE: 11/17/2003

TIME: 15:15:51

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\11172003\J645085.raw

L:388 M:283 W: Missing Blank Line separator, <400> field identifier  
L:395 M:283 W: Missing Blank Line separator, <220> field identifier  
L:399 M:283 W: Missing Blank Line separator, <400> field identifier  
L:442 M:112 C: (48) String data converted to lower case,  
L:461 M:283 W: Missing Blank Line separator, <220> field identifier  
L:465 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1218 M:252 E: No. of Seq. differs, <211> LENGTH:Input:115 Found:108 SEQ:60  
L:1268 M:254 E: No. of Bases conflict, LENGTH:Input:433 Counted:432 SEQ:63  
L:1269 M:252 E: No. of Seq. differs, <211> LENGTH:Input:433 Found:432 SEQ:63  
L:1295 M:254 E: No. of Bases conflict, LENGTH:Input:323 Counted:321 SEQ:64  
L:1297 M:252 E: No. of Seq. differs, <211> LENGTH:Input:323 Found:321 SEQ:64  
L:1311 M:112 C: (48) String data converted to lower case,  
L:1352 M:252 E: No. of Seq. differs, <211> LENGTH:Input:110 Found:102 SEQ:69  
L:16 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (109) Counted (72)